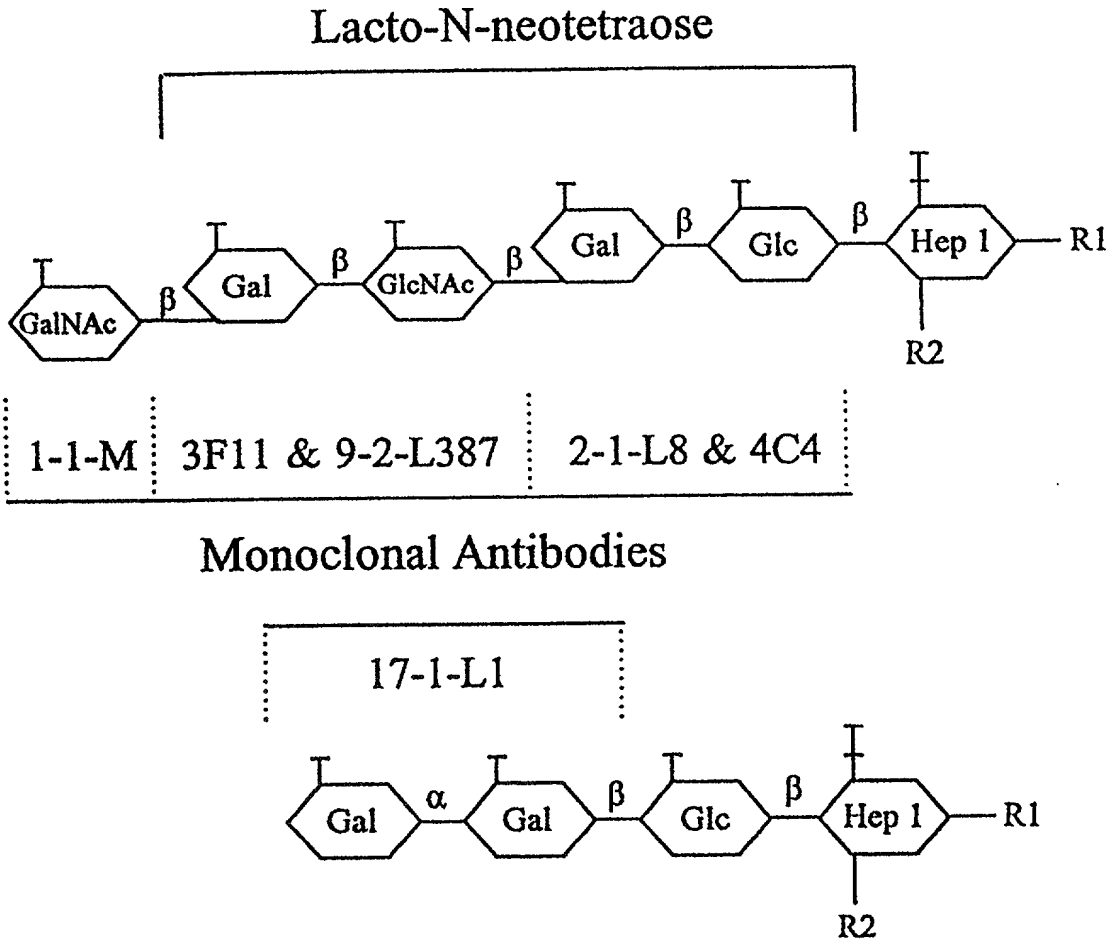

Lacto-N-neotetraose
GalNAc
β
Gal
β
GlcNAc
β
Gal
β
Glc
β
Hep 1
R1
R2
1-1-M
3F11 & 9-2-L387
2-1-L8 & 4C4
Monoclonal Antibodies
17-1-L1
Gal
α
Gal
β
Glc
β
Hep 1
R1
R2

FIG. 1

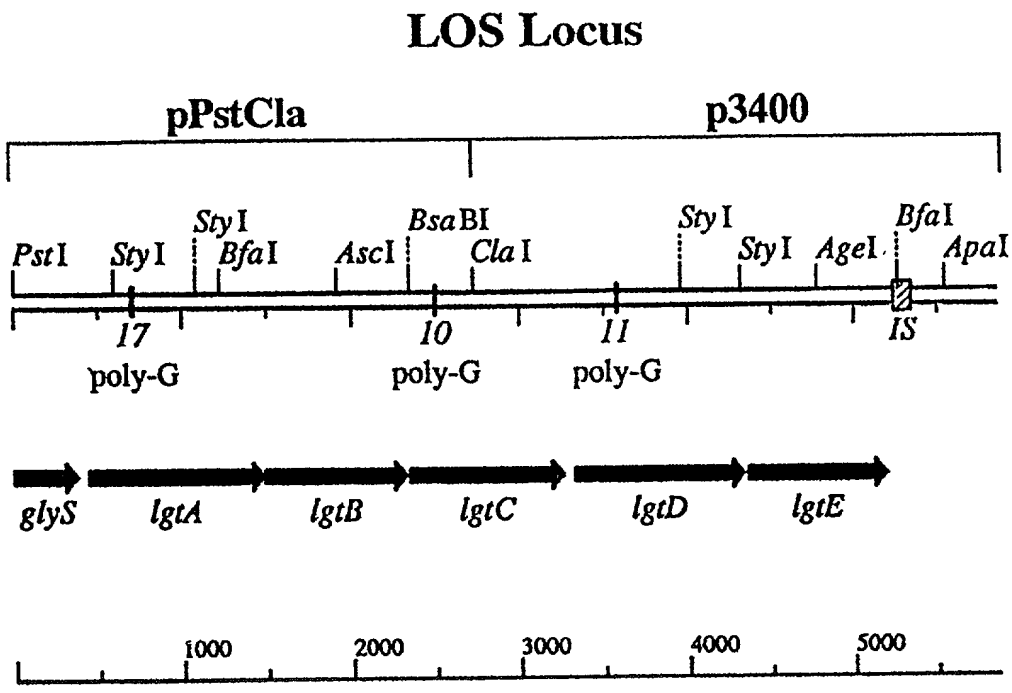

LOS Locus
pPstCla
p3400
PstI
StyI
StyI
BfaI
AscI
BsaBI
ClaI
StyI
StyI
AgeI
BfaI
ApaI
17
poly-G
10
poly-G
11
poly-G
IS
glyS
lgtA
lgtB
lgtC
lgtD
lgtE
1000
2000
3000
4000
5000

FIG.2A

FIG.2B-1

```
SOURCE      Neisseria gonorrhoeae.
ORGANISM    Neisseria gonorrhoeae
     source          1..5859

     CDS             <1..381
                     /gene="glyS"
                     /codon_start=1
                     /transl_table=11
                     /product="glycyl tRNA synthetase beta chain"

/translation="LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQ
DEEKALYAAAQGLQPKIAAAVAEGNFRTALSELASVKPQVDAFFDGVMVMAEDAAVKQ
NRLNLLNRLAEQMNAVADIALLGE"

     CDS             445..1491
                     /gene="lgtA"
                     /codon_start=1
                     /function="adds GlcNAc to lacto-N-neotetraose chain of
                     gonococcal LOS"
                     /evidence=experimental
                     /transl_except=(pos:445..447,aa:Met)
                     /transl_table=11
                     /product="glycosyl transferase"

/translation="MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTD
GTLAIAKDFQKRDSRIKILAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIA
SPGWIEKIVGEMEKDRSIIAMGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAA
FFPFGNPIHNNTMIMRRSVIDGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKY
RLHANQVSSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEK
DLPEEDFERARRFLYQCFKRTDTPPSGAWLDFAADGRMRRLFTLRQYFGILYRLIKNR
RQARSDSAGKEQEI"
```

FIG.2B-2

```
CDS             1491..2330
                /gene="lgtB"
                /codon_start=1
                /function="adds second galactose to the lacto-N-tetraose
                chain in LOS"
                /evidence=experimental
                /product="glycosyl transferase"

/translation="MQNHVISLASAAERRAHIAATFGSRGIPFQFFDALMPSERLERA
MAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLA
EDTWLQERFDPDSAFVVRLETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISR
KAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQN
SALGSLIEHDRRLNRKQQWRDSPANTFKHRLIRALTKIGREREKRRQRREQLIGKIIV
PFQ"

CDS             2342..3262
                /gene="lgtC"
                /codon_start=1
                /function="adds galactose alpha(1-4) to Gal-Glc in
                gonococcal LOS"
                /evidence=experimental
                /trans1_table=11
                /product="glycosyl transferase"

/translation="MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEEN
RAAVAANLRGGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLD
TDVLVRDGLKPLWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINL
KKWRRHDIFKMSCEWVEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMAN
GFASRHTDPLYLDRTNTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEE
WRGKLAVPPTKCMLQRWRKKLSARFLRKIY"
```

FIG.2B-3

```
CDS             3322..4335
                /gene="lgtD"
                /codon_start=1
                /function="adds terminal GalNAc to lacto-N-neotetraose
                chain of LOS"
                /evidence=experimental
                /transl_except=(pos:3322..3324,aa:Met)
                /transl_table=11
                /product="glycosyl transferase"

/translation="MQPLVSVLICAYNAEKYFAQSLAAVVGQTWRNLDILIVDDGSTD
GTPAIARHFQEQDGRIRIISNPRNLGFIASLNIGLDELAKSGGGEYIARTDADDIASP
GWIEKIVGEMEKDRSIIAMGAWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVF
PFGNPIHNNTMIMRRSVIDGGLRFDPAYIHAEDYKFWYEAGKLGRLAYYPEALVKYRF
HQDQTSSKYNLQQRRTAWKIKEEIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKAL
SGQDIGCLRLFLYEYFLSLEKYSLTDLLDFLTDRVMRKLFAAPQYRKILKKMLRPWKY
RSY"
    CDS         4354..5196
                /gene="lgtE"
                /codon_start=1
                /function="adds first galactose to lacto-N-neotetraose
                chain of LOS"
                /evidence=experimental
                /trans1_table=11
                /product="glycosyl transferase"

/translation="MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQA
MAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLA
EDTWLEERFDKDSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISR
EAMRFFLDRFAVLPPERIKAVDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQN
SMLGSDLEKDREQGRRHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRV
ILFK"
```

FIG.2B-4

BASE COUNT 1412 a 1462 c 1661 g 1324 t
ORIGIN

```
   1 ctgcaggccg tcgccgtatt caaacaactg cccgaagccg ccgcgctcgc cgccgccaac
  61 aaacgcgtgc aaaacctgct gaaaaaagcc gatgccgcgt tgggcgaagt caatgaaagc
 121 ctgctgcaac aggacgaaga aaaagccctg tacgctgccg cgcaaggttt gcagccgaaa
 181 attgccgccg ccgtcgccga aggcaatttc cgaaccgcct tgtccgaact ggcttccgtc
 241 aagccgcagg ttgatgcctt cttcgacggc gtgatggtga tggcggaaga tgccgccgta
 301 aaacaaaacc gcctgaacct gctgaaccgc ttggcagagc agatgaacgc ggtggccgac
 361 atcgcgcttt tgggcgagta accgttgtac agtccaaatg ccgtctgaag ccttcaggcg
 421 gcatcaaatt atcgggagag taaattgcag cctttagtca gcgtattgat ttgcgcctac
 481 aacgtagaaa aatattttgc ccaatcatta gccgccgtcg tgaatcagac ttggcgcaac
 541 ttggatattt tgattgtcga tgacggctcg acagacggca cacttgccat tgccaaggat
 601 tttcaaaagc gggacagccg tatcaaaatc cttgcacaag ctcaaaattc cggcctgatt
 661 ccctctttaa acatcgggct ggacgaattg gcaaagtcgg gggggggggg gggggaatat
 721 attgcgcgca ccgatgccga cgatattgcc tcccccggct ggattgagaa aatcgtgggc
 781 gagatggaaa aagaccgcag catcattgcg atgggcgcgt ggctggaagt tttgtcggaa
 841 gaaaaggacg gcaaccggct ggcgcggcac cacaaacacg gcaaaatttg gaaaaagccg
 901 acccggcacg aagacatcgc cgccttttc cctttcggca accccataca caacaacacg
 961 atgattatgc ggcgcagcgt cattgacggc ggtttgcgtt acgacaccga gcgggattgg
1021 gcggaagatt accaattttg gtacgatgtc agcaaattgg gcaggctggc ttattatccc
1081 gaagccttgg tcaaataccg ccttcacgcc aatcaggttt catccaaaca cagcgtccgc
1141 caacacgaaa tcgcgcaagg catccaaaaa accgccagaa acgatttttt gcagtctatg
1201 ggttttaaaa cccggttcga cagcctagaa taccgccaaa caaaagcagc ggcgtatgaa
1261 ctgccggaga aggatttgcc ggaagaagat tttgaacgcg cccgccggtt tttgtaccaa
1321 tgcttcaaac ggacggacac gccgccctcc ggcgcgtggc tggatttcgc ggcagacggc
1381 aggatgaggc ggctgtttac cttgaggcaa tacttcggca ttttgtaccg gctgattaaa
1441 aaccgccggc aggcgcggtc ggattcggca gggaaagaac aggagattta atgcaaaacc
1501 acgttatcag cttggcttcc gccgcagaac gcagggcgca cattgccgca accttcggca
1561 gtcgcggcat cccgttccag tttttcgacg cactgatgcc gtctgaaagg ctggaacggg
```

FIG.2B-5

```
1621 caatggcgga actcgtcccc ggcttgtcgg cgcaccccta tttgagcgga gtggaaaaag
1681 cctgctttat gagccacgcc gtattgtggg aacaggcatt ggacgaaggc gtaccgtata
1741 tcgccgtatt tgaagatgat gtcttactcg gcgaaggcgc ggagcagttc cttgccgaag
1801 atacttggct gcaagaacgc tttgaccccg attccgcctt tgtcgtccgc ttggaaacga
1861 tgtttatgca cgtcctgacc tcgccctccg gcgtggcgga ctacggcggg cgcgcctttc
1921 cgcttttgga aagcgaacac tgcgggacgg cgggctatat tatttcccga aaggcgatgc
1981 gtttttttctt ggacaggttt gccgttttgc cgcccgaacg cctgcaccct gtcgatttga
2041 tgatgttcgg caaccctgac gacagggaag gaatgccggt ttgccagctc aatcccgcct
2101 tgtgcgccca agagctgcat tatgccaagt ttcacgacca aaacagcgca ttgggcagcc
2161 tgatcgaaca tgaccgccgc ctgaaccgca aacagcaatg gcgcgattcc cccgccaaca
2221 cattcaaaca ccgcctgatc cgcgccttga ccaaaatcgg cagggaaagg gaaaaacgcc
2281 ggcaaaggcg cgaacagtta atcggcaaga ttattgtgcc tttccaataa aaggagaaaa
2341 gatggacatc gtatttgcgg cagacgacaa ctatgccgcc taccttgcg ttgcggcaaa
2401 aagcgtggaa gcggcccatc ccgatacgga aatcaggttc cacgtcctcg atgccggcat
2461 cagtgaggaa aaccgggcgg cggttgccgc caatttgcgg gggggggta atatccgctt
2521 tatagacgta aaccccgaag atttcgccgg cttcccctta aacatcaggc acatttccat
2581 tacgacttat gcccgcctga aattgggcga atacattgcc gattgcgaca aagtcctgta
2641 tctggatacg gacgtattgg tcagggacgg cctgaagccc ttatgggata ccgatttggg
2701 cggtaactgg gtcggcgcgt gcatcgattt gtttgtcgaa aggcaggaag gatacaaaca
2761 aaaaatcggt atggcggacg gagaatatta tttcaatgcc ggcgtattgc tgatcaacct
2821 gaaaaagtgg cggcggcacg atattttcaa aatgtcctgc gaatgggtgg aacaatacaa
2881 ggacgtgatg caatatcagg atcaggacat tttgaacggg ctgtttaaag gcggggtgtg
2941 ttatgcgaac agccgtttca actttatgcc gaccaattat gcctttatgg cgaacgggtt
3001 tgcgtcccgc cataccgacc cgctttacct cgaccgtacc aatacggcga tgcccgtcgc
3061 cgtcagccat tattgcggct cggcaaagcc gtggcacagg gactgcaccg tttggggtgc
3121 ggaacgtttc acagagttgg ccggcagcct gacgaccgtt cccgaagaat ggcgcggcaa
3181 acttgccgtc ccgccgacaa agtgtatgct tcaaagatgg cgcaaaaagc tgtctgccag
3241 attcttacgc aagatttatt gacggggcag gccgtctgaa gccttcagac ggcatcggac
3301 gtatcggaaa ggagaaacgg attgcagcct ttagtcagcg tattgatttg cgcctacaac
3361 gcagaaaaat attttgccca atcattggcc gccgtagtgg ggcagacttg gcgcaacttg
```

FIG.2B-6

```
3421 gatattttga ttgtcgatga cggctcgacg gacggcacgc ccgccattgc ccggcatttc
3481 caagaacagg acggcaggat caggataatt tccaatcccc gcaatttggg ctttatcgcc
3541 tctttaaaca tcgggctgga cgaattggca aagtcggggg ggggggaata tattgcgcgc
3601 accgatgccg acgatattgc ctcccccggc tggattgaga aaatcgtggg cgagatggaa
3661 aaagaccgca gcatcattgc gatgggcgcg tggttggaag ttttgtcgga agaaaacaat
3721 aaaagcgtgc ttgccgccat tgcccgaaac ggcgcaattt gggacaaacc gacccggcat
3781 gaagacattg tcgccgtttt ccctttcggc aaccccatac acaacaacac gatgattatg
3841 aggcgcagcg tcattgacgg cggtttgcgg ttcgatccag cctatatcca cgccgaagac
3901 tataagtttt ggtacgaagc cggcaaactg ggcaggctgg cttattatcc cgaagccttg
3961 gtcaaatacc gcttccatca agaccagact tcttccaaat acaacctgca acagcgcagg
4021 acggcgtgga aaatcaaaga agaaatcagg gcggggtatt ggaaggcggc aggcatagcc
4081 gtcggggcgg actgcctgaa ttacgggctt ttgaaatcaa cggcatatgc gttgtacgaa
4141 aaagccttgt ccggacagga tatcggatgc ctccgcctgt tcctgtacga atatttcttg
4201 tcgttggaaa agtattcttt gaccgatttg ctggatttct tgacagaccg cgtgatgagg
4261 aagctgtttg ccgcaccgca atataggaaa atcctgaaaa aaatgttacg cccttggaaa
4321 taccgcagct attgaaaccg aacaggataa atcatgcaaa accacgttat cagcttggct
4381 tccgccgcag agcgcagggc gcacattgcc gataccttcg gcagtcgcgg catcccgttc
4441 cagtttttcg acgcactgat gccgtctgaa aggctggaac aggcgatggc ggaactcgtc
4501 cccggcttgt cggcgcaccc ctatttgagc ggagtggaaa aagcctgctt tatgagccac
4561 gccgtattgt gggaacaggc gttggatgaa ggtctgccgt atatcgccgt atttgaggac
4621 gacgttttac tcggcgaagg cgcggagcag ttccttgccg aagatacttg gttggaagag
4681 cgttttgaca aggattccgc ctttatcgtc cgtttggaaa cgatgtttgc gaaagttatt
4741 gtcagaccgg ataaagtcct gaattatgaa aaccggtcat ttcctttgct ggagagcgaa
4801 cattgtggga cggctggcta tatcatttcg cgtgaggcga tgcggttttt cttggacagg
4861 tttgccgttt tgccgccaga gcggattaaa gcggtagatt tgatgatgtt tacttatttc
4921 tttgataagg aggggatgcc tgtttatcag gttagtcccg ccttatgtac ccaagaattg
4981 cattatgcca agtttctcag tcaaaacagt atgttgggta gcgatttgga aaaagatagg
5041 gaacaaggaa gaagacaccg ccgttcgttg aaggtgatgt ttgacttgaa gcgtgctttg
5101 ggtaaattcg gtagggaaaa gaagaaaaga atggagcgtc aaaggcaggc ggagcttgag
5161 aaagtttacg gcaggcgggt catattgttc aaatagtttg tgtaaaatat aggggattaa
```

FIG.2B-7

```
5221 aatcagaaat ggacacactg tcattcccgc gcaggcggga atctaggtct ttaaacttcg
5281 gtttttttccg ataaattctt gccgcattaa aattccagat tcccgctttc gcggggatga
5341 cggcgggggg attgttgctt tttcggataa aatcccgtgt tttttcatct gctaggtaaa
5401 atcgccccaa agcgtctgca tcgcggcgat ggcggcgagt ggggcggttt ctgtgcgtaa
5461 aatccgtttt ccgagtgtaa ccgcctgaaa gccggcttca aatgcctgtt gttcttcctg
5521 ttctgtccag ccgccttcgg gcccgaccat aaagacgatt gcgccggacg ggtggcggat
5581 gtcgccgagt ttgcaggcgc ggttgatgct cataatcagc ttggtgtttt cagacggcat
5641 tttgtcgagt gcttcacggt agccgatgat gggcagtacg gggggaacgg tgttcctgcc
5701 gctttgttcg cacgcggaga tgacgatttc ctgccagcgt gcgaggcgtt tggcggcgcg
5761 ttctccgtcg aggcggacga tgcagcgttc gctgatgacg ggctgtatgg cggttacgcc
5821 gagttcgacg ctttttttgca gggtgaaatc catgcgatc
```

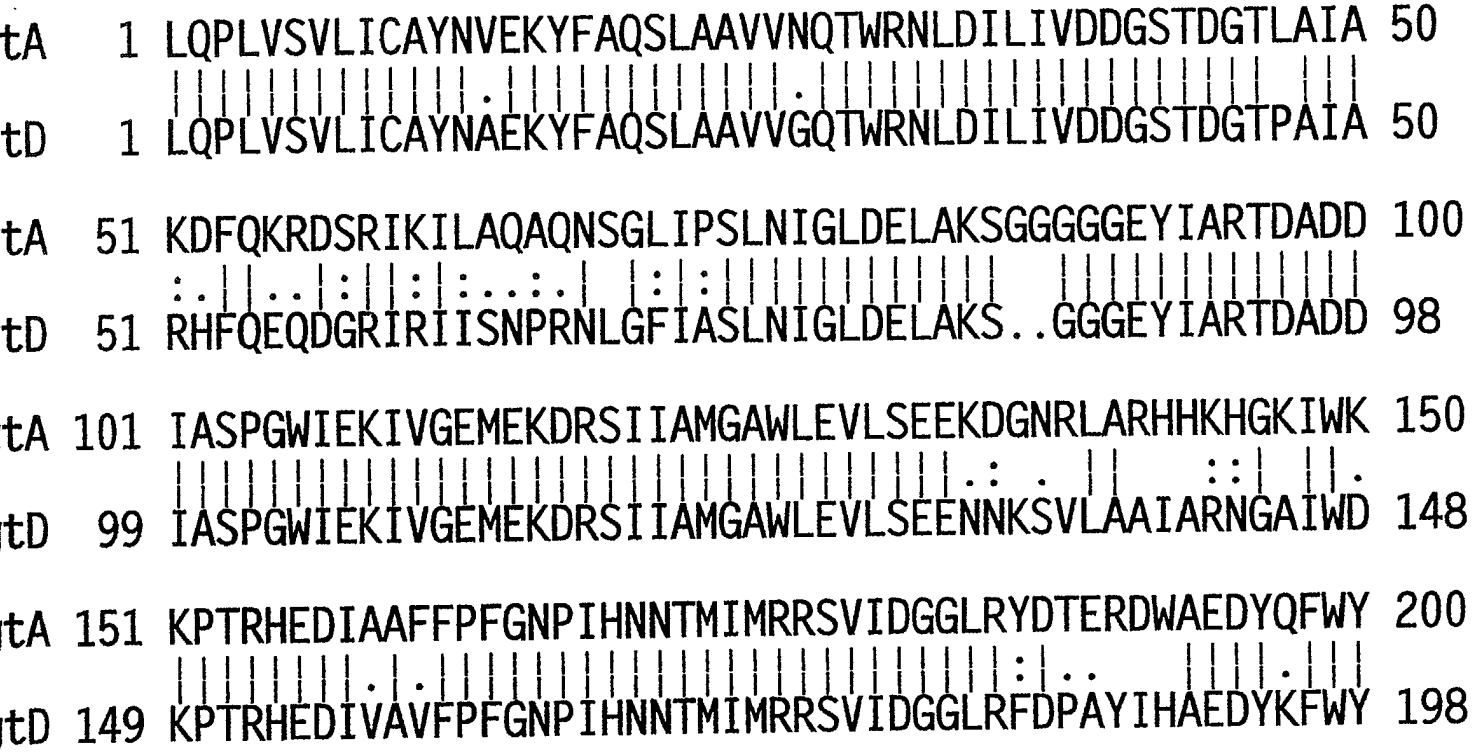


FIG.3A

```
lgtA 201 DVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGIQKTARNDFLQ 250
         :.:|||||||||||||||||:|.:|.|||.:.:.|: .|  |... |.:::.
lgtD 199 EAGKLGRLAYYPEALVKYRFHQDQTSSKYNLQQRRTAWKIKEEIRAGYWK 248

lgtA 251 SMGFKTRFDSLEYRQTKAAAYELPEKDLPEEDFERARRFLYQCFKRTDTP 300
         . |: .  |:|:|  |..|||.| ||.|.::|::  | ||||::| . :.
lgtD 249 AAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLEKY 298

lgtA 301 PSGAWLDFAADGRMRRLFTLRQYFGILYRLIKNRR 335
         . ..:|||.|  ||:||. .||  || :::: ::
lgtD 299 SLTDLLDFLTDRVMRKLFAAPQYRKILKKMLRPWK 333
```

FIG.3B

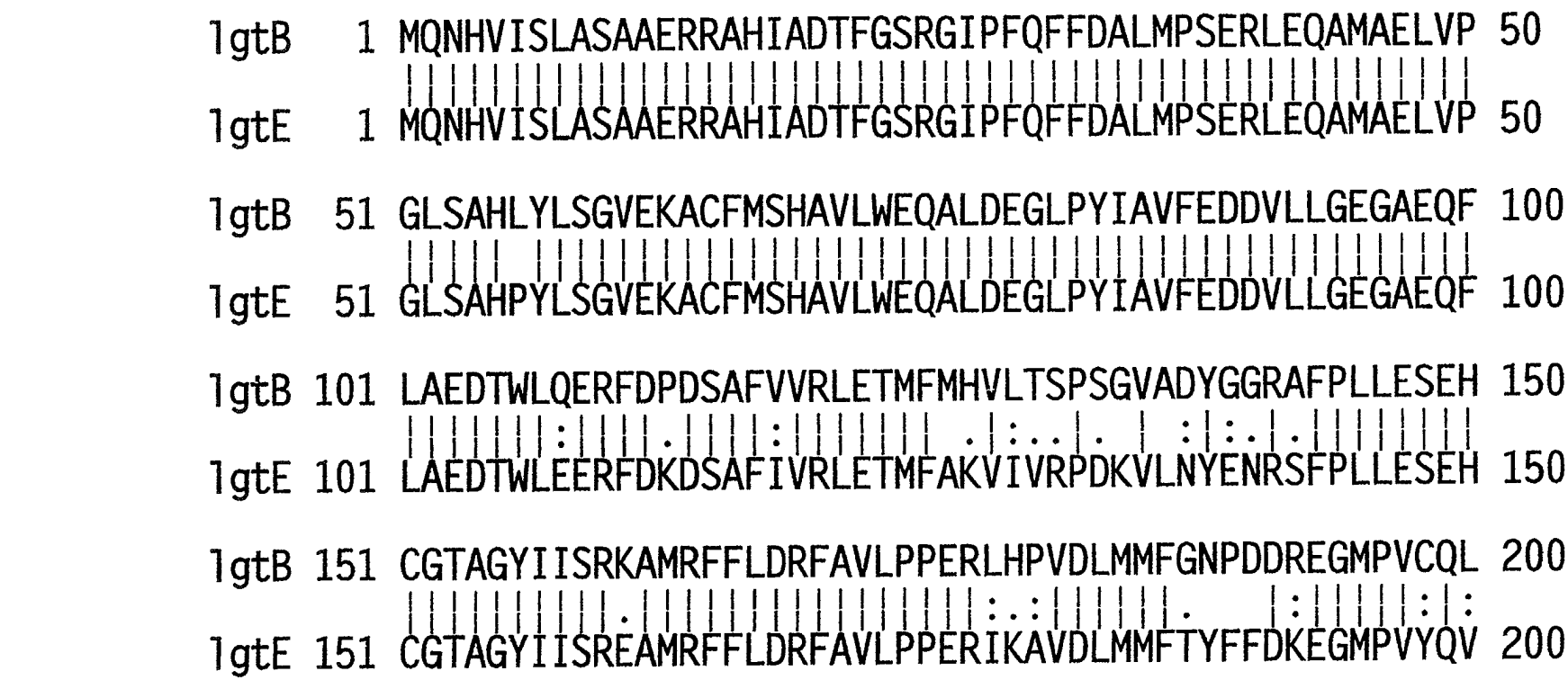

lgtB 1 MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVP 50
lgtE 1 MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVP 50
lgtB 51 GLSAHLYLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQF 100
lgtE 51 GLSAHPYLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQF 100
lgtB 101 LAEDTWLQERFDPDSAFVVRLETMFMHVLTSPSGVADYGGRAFPLLESEH 150
lgtE 101 LAEDTWLEERFDKDSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEH 150
lgtB 151 CGTAGYIISRKAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQL 200
lgtE 151 CGTAGYIISREAMRFFLDRFAVLPPERIKAVDLMMFTYFFDKEGMPVYQV 200

FIG.4A

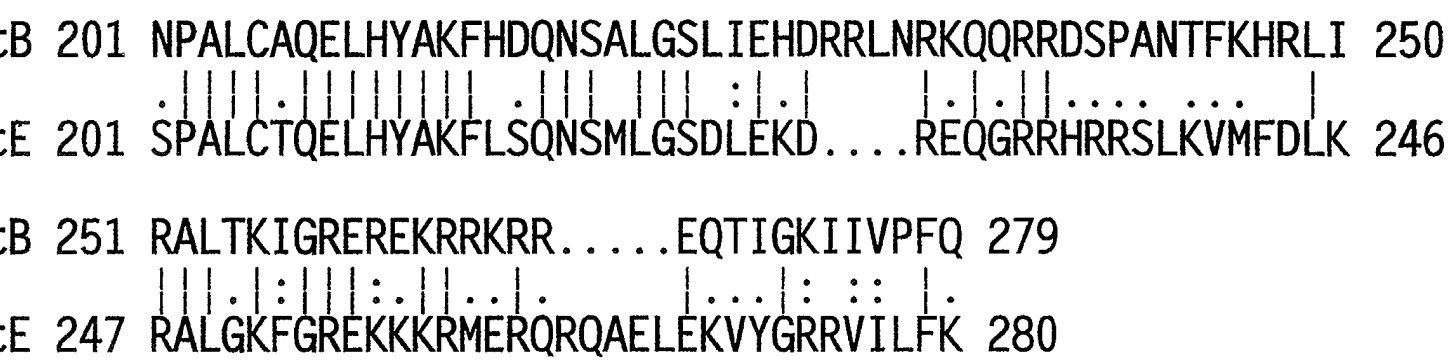

lgtB 201 NPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQRRDSPANTFKHRLI 250
lgtE 201 SPALCTQELHYAKFLSQNSMLGSDLEKD....REQGRRHRRSLKVMFDLK 246
lgtB 251 RALTKIGREREKRRKRR.....EQTIGKIIVPFQ 279
lgtE 247 RALGKFGREKKKRMERQRQAELEKVYGRRVILFK 280

FIG.4B

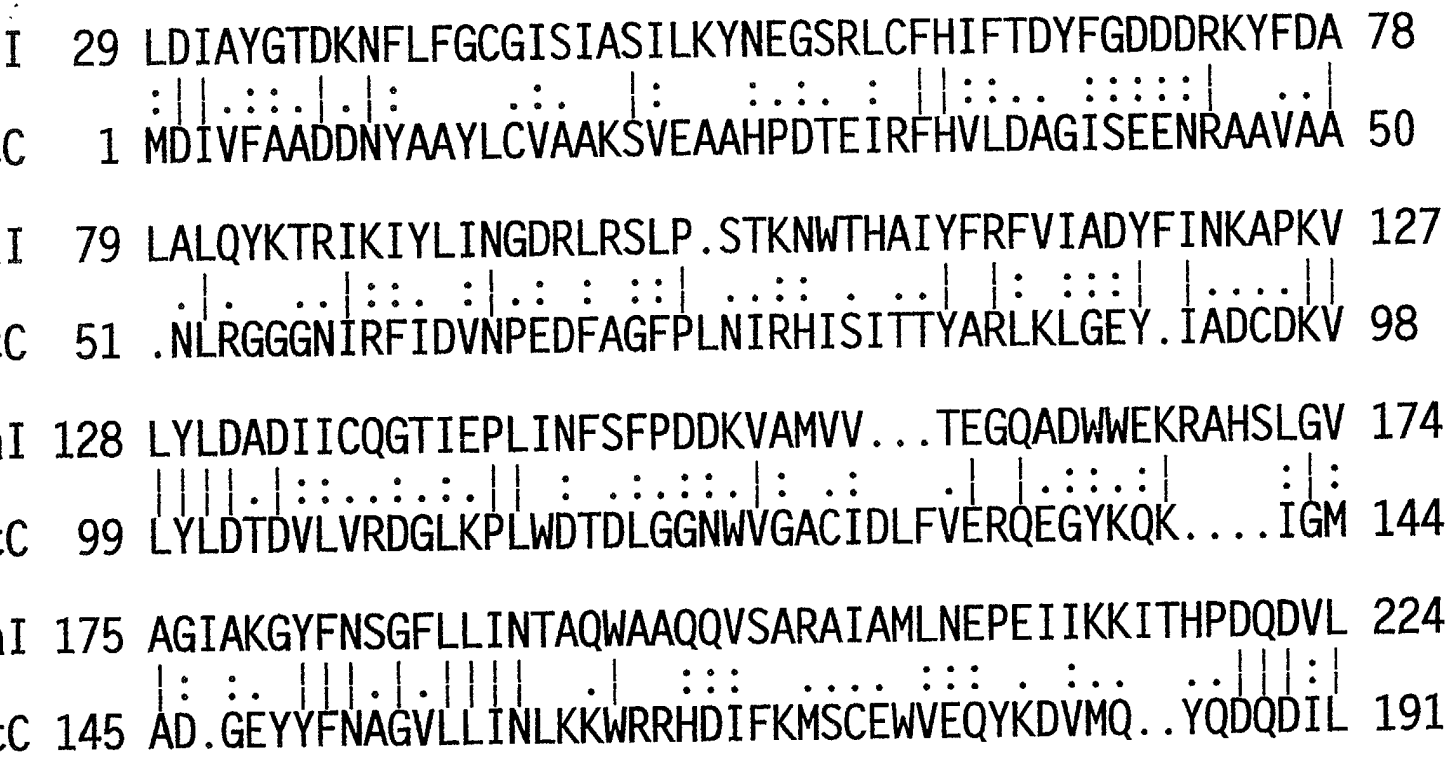
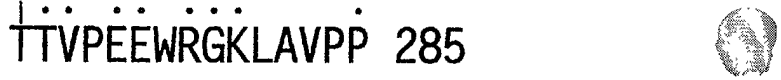

rfaI 29 LDIAYGTDKNFLFGCGISIASILKYNEGSRLCFHIFTDYFGDDDRKYFDA 78
lgtC 1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAA 50
rfaI 79 LALQYKTRIKIYLINGDRLRSLP.STKNWTHAIYFRFVIADYFINKAPKV 127
lgtC 51 .NLRGGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEY.IADCDKV 98
rfaI 128 LYLDADIICQGTIEPLINFSFPDDKVAMVV...TEGQADWWEKRAHSLGV 174
lgtC 99 LYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVERQEGYKQK....IGM 144
rfaI 175 AGIAKGYFNSGFLLINTAQWAAQQVSARAIAMLNEPEIIKKITHPDQDVL 224
lgtC 145 AD.GEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYKDVMQ..YQDQDIL 191

FIG.5A



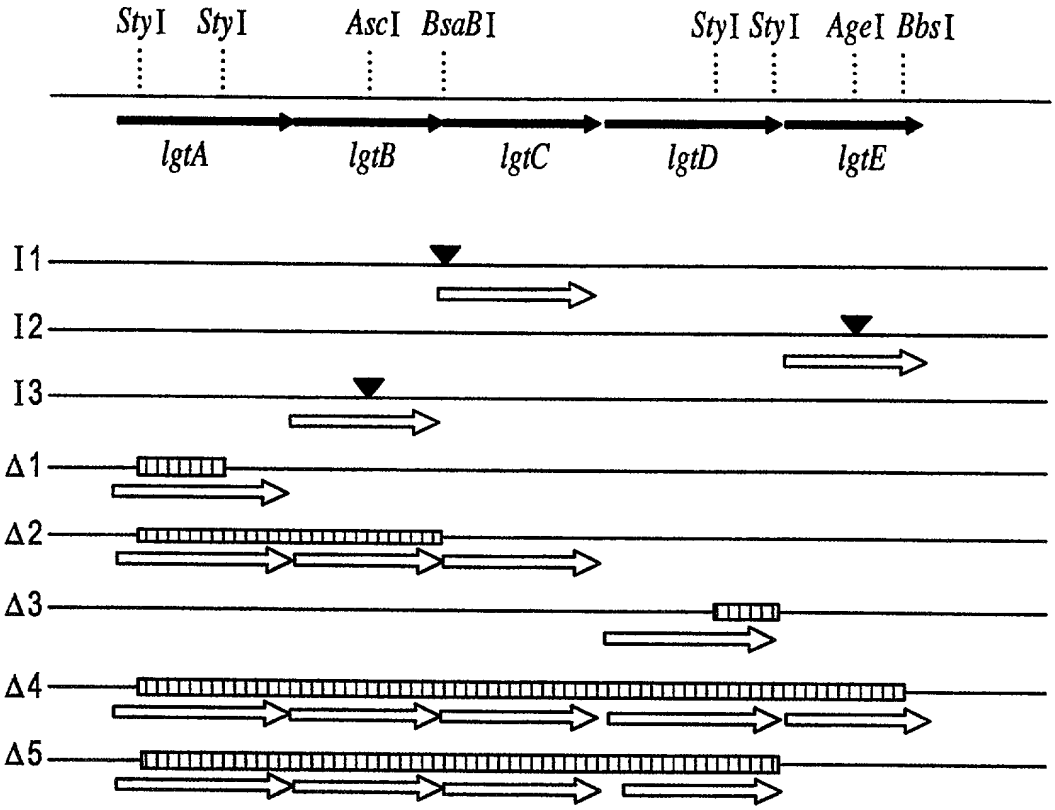

```
rfaI 225 NMLLADKLIFADIKYNTQFSLNYQLKESFINPVTNDTIFI..... 264
         |  |:  :  :.:|: ::|   :.  ||.:... :..   .|.:::
lgtC 192 NGLFKGGVCYANSRFNF.MPTNYAFMANGFASRHTDPLYLDRTNTAMPVA 240

rfaI 265 ..HYIGPTKPWHDWAWDYPVSQAFMEAKNASPWKNTALLKPNNSNQLRYS 312
           ||.|..||||    :|:.|..|  .  .. |:.:   |.:  ..  .:.      .
lgtC 241 VSHYCGSAKPWH...RDCTVWGAERFTELAGSL..TTVPEEWRGKLAVPP 285

rfaI 313 AKHMLKKHRYLKGFSNYLFYFI 334
         .|  ||   :|:  |  :|.  ::   |
lgtC 286 TKCML..QRWRKKLSARFLRKI 305
```

FIG.5B

FIG.6


StyI
StyI
AscI
BsaBI
StyI
StyI
AgeI
BbsI
lgtA
lgtB
lgtC
lgtD
lgtE
I1
I2
I3
Δ1
Δ2
Δ3
Δ4
Δ5

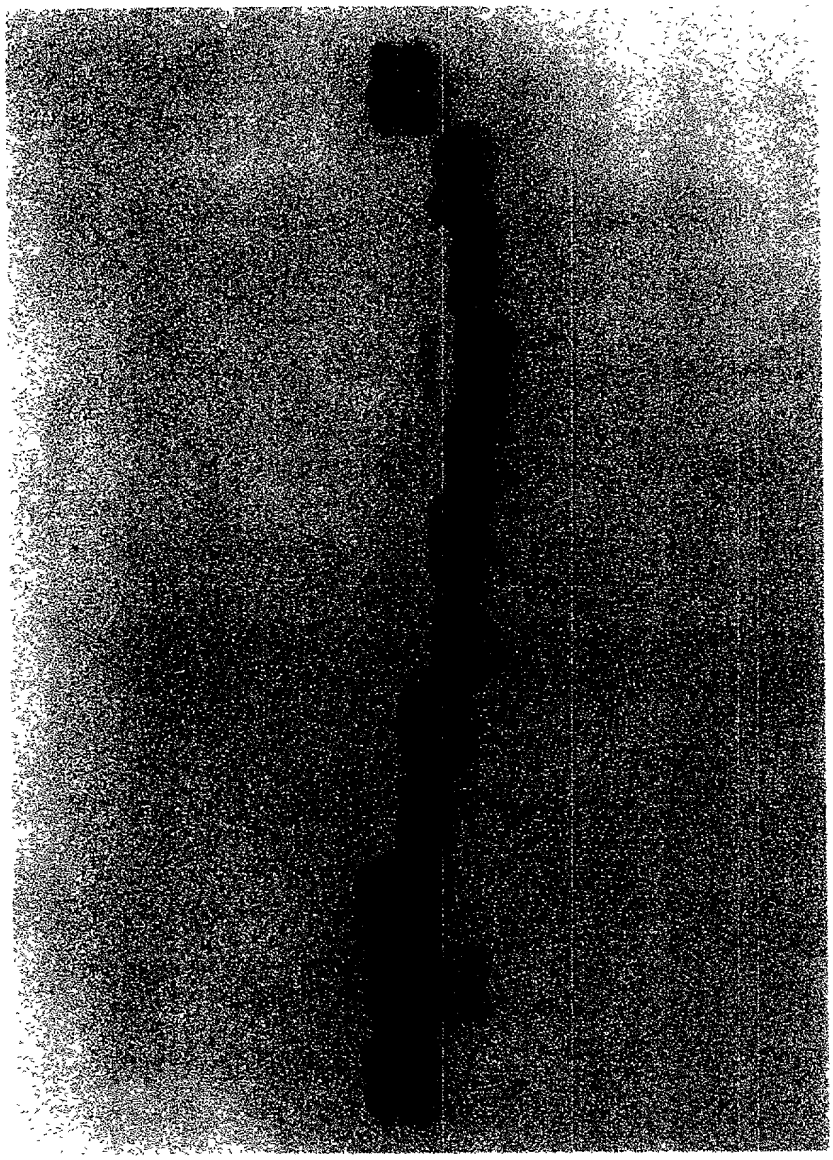


FIG. 7

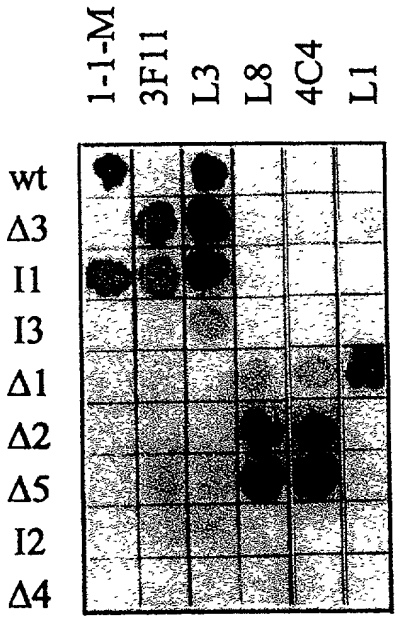


FIG.8